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**ENTERED**



OIIPE

## RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/10/083,842A

TIME: 13:13:47

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\06032002\J083842A.raw

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3 <110> APPLICANT: Syngenta Biotechnology, Inc.
4   Grina, Jonas
6 <120> TITLE OF INVENTION: NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE
7   EXPRESSION IN PLANTS OR ANIMALS
9 <130> FILE REFERENCE: 1392/2/2
11 <140> CURRENT APPLICATION NUMBER: US/10/083,842A
C--> 12 <141> CURRENT FILING DATE: 2002-05-21
14 <150> PRIOR APPLICATION NUMBER: 60/272,905
15 <151> PRIOR FILING DATE: 2001-03-02
17 <160> NUMBER OF SEQ ID NOS: 12
19 <170> SOFTWARE: PatentIn version 3.0
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22 <211> LENGTH: 17
23 <212> TYPE: DNA
C--> 24 <213> ORGANISM: Artificial
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27 <223> OTHER INFORMATION: primer containing synthetic TATA box
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (1)..(17)
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48 <221> NAME/KEY: misc_feature
49 <222> LOCATION: (1)..(17)
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58 <211> LENGTH: 36
59 <212> TYPE: DNA
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62 <220> FEATURE:
63 <223> OTHER INFORMATION: PCR primer for amplification of Drosophila melanogaster DNA
65 <220> FEATURE:
66 <221> NAME/KEY: misc_feature

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67 <222> LOCATION: (1)..(36)
68 <223> OTHER INFORMATION: PCR primer for amplification of Drosophila melanogaster DNA
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76 <211> LENGTH: 36
77 <212> TYPE: DNA
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83 <220> FEATURE:
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85 <222> LOCATION: (1)..(36)
86 <223> OTHER INFORMATION: PCR primer for amplification of Drosophila melanogaster DNA
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98 <220> FEATURE:
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112 aagtgcattg aacccttgct tcggatc 147
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117 <212> TYPE: DNA
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129 aacctccgct tccacatcac cgagcgaact ctagaactcg cgtactcttc tcacctgttg 120
131 cttcggattg tggttgact gaaaagcgac gcgtatcgtg gtcgaagatt ctctataagt 180
133 gcataatata ttcgagacag tggatagcga ttcgtttcgg tttcatcgcg cggatgagtg 240
135 gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaagcc 300
137 tacgtcagag gatgtccctc ggtggtcacg gaagccgggg cgtgtgacgc gctcttcgac 360
139 atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt 408
140 Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
141 1 5 10 15
143 gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg 456

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144	Glu	Glu	Ser	Ser	Ser	Glu	Val	Thr	Ser	Ser	Ser	Ala	Phe	Gly	Met	Pro	
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147	gcg	gcc	atg	gta	atg	tca	ccg	gag	tcg	ctg	gcg	tcg	cca	gag	tac	ggc	504
148	Ala	Ala	Met	Val	Met	Ser	Pro	Glu	Ser	Leu	Ala	Ser	Pro	Glu	Tyr	Gly	
149			35				40					45					
151	ggc	ctc	gag	ctc	tgg	agc	tac	gat	gag	acc	atg	aca	aac	tat	ccg	gcg	552
152	Gly	Leu	Glu	Leu	Trp	Ser	Tyr	Asp	Glu	Thr	Met	Thr	Asn	Tyr	Pro	Ala	
153		50					55				60						
155	cag	tca	ctg	ctc	ggc	gcg	tgt	aat	gcg	ccg	cag	cag	cag	cag	caa	cag	600
156	Gln	Ser	Leu	Leu	Gly	Ala	Cys	Asn	Ala	Pro	Gln	Gln	Gln	Gln	Gln	Gln	
157	65				70				75						80		
159	caa	caa	cag	cag	ccg	tcc	gct	cag	ccg	ctg	ccg	tct	atg	ccg	ctg	ccg	648
160	Gln	Gln	Gln	Gln	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Ser	Met	Pro	Leu	Pro	
161					85				90						95		
163	atg	cct	cct	aca	act	cct	aaa	tca	gag	aac	gag	tcc	atg	tcg	tca	ggt	696
164	Met	Pro	Pro	Thr	Thr	Pro	Lys	Ser	Glu	Asn	Glu	Ser	Met	Ser	Ser	Gly	
165				100					105					110			
167	cga	gaa	gaa	tta	tca	ccg	gcc	tca	agt	ata	aat	gga	tgt	agt	act	gat	744
168	Arg	Glu	Glu	Leu	Ser	Pro	Ala	Ser	Ser	Ile	Asn	Gly	Cys	Ser	Thr	Asp	
169			115				120						125				
171	ggg	gaa	cca	aga	cga	cag	aag	aaa	ggg	cca	gcg	ccg	cgc	cag	cag	gag	792
172	Gly	Glu	Pro	Arg	Arg	Gln	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Gln	Gln	Glu	
173		130				135					140						
175	gaa	ctg	tgc	ctt	gtt	tgc	ggc	gac	agg	gct	tcg	gga	tat	cac	tat	aac	840
176	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	
177	145				150				155						160		
179	gcg	ctt	acg	tgc	gaa	gga	tgt	aaa	ggg	ttc	ttc	agg	cgg	agt	gtg	acc	888
180	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Thr	
181				165					170						175		
183	aag	aat	gcg	gta	tat	att	tgt	aaa	ttt	gga	cac	gcc	tgc	gag	atg	gac	936
184	Lys	Asn	Ala	Val	Tyr	Ile	Cys	Lys	Phe	Gly	His	Ala	Cys	Glu	Met	Asp	
185			180						185					190			
187	atg	tac	atg	agg	aga	aaa	tgc	caa	gag	tgt	cgg	ttg	aag	aaa	tgc	ctc	984
188	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	
189			195				200						205				
191	gcg	gtg	ggc	atg	agg	ccc	gag	tgc	gtc	gtc	cca	gag	tcc	acg	tgc	aag	1032
192	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Ser	Thr	Cys	Lys	
193		210					215					220					
195	aac	aaa	aga	aga	gaa	aag	gaa	gca	cag	aga	gaa	aaa	gac	aaa	ctg	cca	1080
196	Asn	Lys	Arg	Arg	Glu	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Leu	Pro	
197	225				230						235				240		
199	gtc	agt	acg	acg	aca	gtg	gac	gat	cat	atg	cct	gcc	ata	atg	caa	tgt	1128
200	Val	Ser	Thr	Thr	Val	Asp	Asp	His	Met	Pro	Ala	Ile	Met	Gln	Cys		
201				245					250					255			
203	gac	cct	ccg	ccc	cca	gag	gcg	gca	agg	att	cac	gaa	gtg	gtc	ccg	agg	1176
204	Asp	Pro	Pro	Pro	Pro	Glu	Ala	Ala	Arg	Ile	His	Glu	Val	Val	Pro	Arg	
205			260						265					270			
207	ttc	cta	acg	gag	aag	cta	atg	gag	cag	aac	aga	ctg	aag	aat	gtg	acg	1224
208	Phe	Leu	Thr	Glu	Lys	Leu	Met	Glu	Gln	Asn	Arg	Leu	Lys	Asn	Val	Thr	

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211 ccg ctg tcg gcg aac cag aag tcc ctg atc gcg agg ctc gtg tgg tac				1272
212 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr				
213 290	295	300		
215 cag gag ggg tac gag cag ccg tcg gag gaa gat ctc aag aga gtt aca				1320
216 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr				
217 305	310	315	320	
219 cag aca tgg cag tta gaa gaa gaa gag gag gaa act gac atg ccc				1368
220 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Thr Asp Met Pro				
221 325	330	335		
223 ttc cgt cag atc aca gag atg acg atc tta aca gtg cag ctt att gta				1416
224 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val				
225 340	345	350		
227 gaa ttc gca aag gga cta ccg gga ttc tcc aag ata tct cag tcc gat				1464
228 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp				
229 355	360	365		
231 caa att aca tta tta aag gcg tca tca agc gaa gtg atg atg ctg cga				1512
232 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg				
233 370	375	380		
235 gtg gcg cga cgg tac gac gcg gcg acg gac agc gtg ctg ttc gcg aac				1560
236 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn				
237 385	390	395	400	
239 aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac				1608
240 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr				
241 405	410	415		
243 gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc				1656
244 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser				
245 420	425	430		
247 atg gac aat gtg cac tac gcg ctg ctc acc gcc atc gtt ata ttc tca				1704
248 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser				
249 435	440	445		
251 gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga				1752
252 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg				
253 450	455	460		
255 tac tac ttg aag acg ctg cgg gtt tac att tta aat cag cac agc gcg				1800
256 Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala				
257 465	470	475	480	
259 tcg cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg				1848
260 Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr				
261 485	490	495		
263 gaa ctg cgc acg ctc ggc acg cag aac tcc aac atg tgc atc tcg ctg				1896
264 Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu				
265 500	505	510		
267 aag ctg aag aac agg aaa ctt ccg cca ttc ctc gag gag atc tgg gac				1944
268 Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp				
269 515	520	525		
271 gtg gcc gaa gtg tcg acg acg cag ccg acg ccg ggg gtg gcg gcg cag				1992
272 Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln				
273 530	535	540		

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276 Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu
277 545 550 555
279 ggcgcgcgcg cccgcgcgcc ccgcgcgcgc cgctcccccg cgccgcgcgc gcgcgcgcgc 2101
281 gcgcgcctgc ctgagtgcgg gaccgcgcgc gagagagaa cgctcataga ctggctagtt 2161
283 ttagtgaagt gcacggacgc gatcgtggga ccgcatcgac gcgtccgtga ggacagtga 2221
285 aatattaccg ctagggcgcg ttctgtacgtg tccggtgacc gacgacgatg atgcgcgtga 2281
287 gattagtga tatatgtgtt gttgaacgtt tggagagtat atttagtgtt gatcgtcggg 2341
289 agcgcgcgcg cggcgcgtgt cggcgcgcgc tccgcgcgcg gccgcgcgcg gcgactccgc 2401
291 gtttttttcg tttgcgaccg gaaaccgagt cggtcactcg gatacgcccg tatgataaga 2461
293 cttcttttca taaataagtt cacctgtatt gcgcgtacat acgagaatta taaagaaaaa 2521
295 aagtaataata tgaagagatg tttctattgg gtgaaaagtt taaacttatg tttatttacc 2581
297 aaaattaact atacgttgat cgaccttttg actataatat tgtgctgggt cgttggcagc 2641
299 ggccgcagaa cgcgcgcgca ccataattgt ttatatatag tttatgtgag acgttatcgt 2701
301 gtcgtgtcca cttagtcccg attcatgttc caccaggtcg gtgtagtgat cagggcgggc 2761
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305 ttgggagacg ttattcctc 2840
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309 <211> LENGTH: 556
310 <212> TYPE: PRT
311 <213> ORGANISM: Manduca sexta
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323 Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
324 35 40 45
327 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala
328 50 55 60
331 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln Gln
332 65 70 75 80
335 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro
336 85 90 95
339 Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly
340 100 105 110
343 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp
344 115 120 125
347 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
348 130 135 140
351 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn
352 145 150 155 160
355 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr
356 165 170 175
359 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp
360 180 185 190
363 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu
364 195 200 205
367 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\PTO.VSK.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,8,9,10,11,12

## VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:42 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:60 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:78 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:96 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:458 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:476 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:494 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:512 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
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